REMARKS

I. Group Election

The Examiner has restricted the present Application into 3 different groups relating to canine interleukin-5 (IL-5) nucleic acid molecules, methods to regulate an immune response using compositions comprising such nucleic acid molecules and methods to produce a canine IL-5 protein using the disclosed nucleic acid molecules. Specifically, Group I, consisting of claims 1-13, is drawn to canine IL-5 nucleic acid molecules. Immunoregulatory nucleic acid molecules of Group I include SEQ ID NO:1-4, SEQ ID NO:6-9, SEQ ID NO:11-19 and SEQ ID NO:21. Proteins encoded by such nucleic acid molecules include SEQ ID NO:5, SEQ ID NO:10 and SEQ ID NO:20.

Applicants traverse the restriction between Groups I, II and III to the extent that Groups II and III recite the subject matter of Group I. Applicants submit the subject matter of these Groups is sufficiently small and so closely related that a thorough search for the subject matter of Group I would be sufficient to uncover subject matter related to Groups II and III. Specifically, the claims of Group II are drawn to methods to regulate an immune response using the nucleic acids of Group I and compositions thereof. Applicants emphasize the methods of Group II require the use of the nucleic acid acids of Group I and therefore a search of the subject matter for either Group would be sufficient to examine the subject matter of the related Group. Similarly, with regard to Group III, the subject matter of which is methods to produce an immunoregulatory molecule by culturing a cell comprising the disclosed nucleic acid sequences, Applicants submit the methods of Group III also require the use of the nucleic acid molecules of Group I. In fact, Applicants submit that if the sequence identifiers of Group I are removed as elements from the claims of Group III, the claims of Group III lose all meaning. As such, the nucleic acid molecules of Group I are essential for the methods of the claims of Group III. Therefore, Applicants contend that because the methods of Groups II and II cannot be practiced without the nucleic acid molecules of Group I, these Groups do not describe independent inventions as described in M.P.E.P. §802.01 and therefore, Applicants request rejoinder of these Groups.

claims of Group I, and to request that the claims of Groups II and III that depend from or otherwise include all the limitations of the allowable product be rejoined and examined for patentability. *In re Brouwer*, 37 USPQ2d 1663 (Fed. Cir. 1996); *In re Ochiai*, 37 USPQ2d 1127 (Fed. Cir. 1995).

II. Election of Sequences for Examination

The Examiner has further divided the disclosed sequences into 3 independent and distinct Inventions and has required the applicants to elect a single Invention for examination. The sequences have been divided as follows:

Invention I - nucleic acid sequences not containing a part of SEQ ID NO:4 and 6.
Invention II - nucleic acid sequences not containing a part of SEQ ID NO:7 and 8.
Invention III - nucleic acid sequences not containing a part of SEQ ID NO:9 and 11.

Applicants have reviewed the individual Inventions as described by the Examiner but are confused as to the reasoning applied in creating the division between Inventions. In particular, Applicants are confused by the language used to describe the subject matter of each Invention in that such language excludes the majority of the sequence for which the Applicants seek protection. Applicants respectfully submit the Examiner erred in the choice of language, in particular by including the word 'not' in the description, and, further, Applicants believe the Examiner meant to describe each Inventions using inclusive language as follows:

Revised Invention Definition

Invention I - nucleic acid sequences containing a part of SEQ ID NO:4 and 6.
Invention II - nucleic acid sequences containing a part of SEQ ID NO:7 and 8.
Invention III - nucleic acid sequences containing a part of SEQ ID NO:9and 11.

In drafting the response below, Applicants have used the revised Invention definitions given above. Applicants request that if their interpretation of the Examiners intentions is incorrect, and [illegible] the Examiner clarify the

In response to the requirement to elect an Invention, Applicants provisionally elect Invention I with traverse for the following reasons. The Examiner has divided the sequences disclosed in the instant Application into 3 distinct Inventions, as described above. However, Applicants note the disclosed sequences all come from the same canine gene and in fact, many of the sequences are sub-sequences or fragments of the parent sequence and that all of these sequences are identical in their overlapping regions. For the Examiner's convenience, a chart showing the relationship between the claimed sequences is shown below:

SEQ ID NO:	Description
1	primer (m) ATGCACTTT...
2	primer (n) CTGGAGGAA...
3	primer (o) GTGACYCTT...
4	transcript containing canine IL-5 coding region
5	translation of coding region from SEQ ID NO:4
6	reverse complement of SEQ ID NO:4
7	coding sequence for canine IL-5 protein
8	reverse complement of SEQ ID NO:7
9	coding sequence for mature canine IL-5 protein (minus signal sequence)
10	translation of SEQ ID NO:9
11	reverse complement of SEQ ID NO:9
12	primer (p) GGGCTCGAG
13	PRIMER (q) CCCGCGGCC
14	5' AGGCAAACACTGAACATTTC 3'
15	5' TCTCCAAAATCTTCCACTAC 3'
16	5' TCAAGGGAGGCTATAAATTC 3'
17	5' TTATAGTCAAGGGCATATCC 3'
18	sequence of entire canine IL-5 gene including introns
19	reverse complement of SEQ ID NO:18
20	N-terminal 15 amino acids from canine IL-5 protein
21	partially processed transcript

From this chart it can be seen that all of sequences are canine IL-5 sequences, some are full length transcripts or their complements while others are segments of the full length gene (such as SEQ ID NO:9 which is the coding sequence for the mature form of the IL-5 protein), or primers used to generate such nucleic acid molecules. SEQ ID NO:18 is the full length gene including the introns. To further illustrate the identical nature of the major sequences, Applicants have provided an alignment of SEQ ID NO (SIN) 4, 7, 9 and 21:

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SIN4   1 caAGGCAAAC ACTGAACATT TCAGAGCTAT GAGAATGCTT CTGAATTTGA
SIN7   1 ---------- ---------- --------AT GAGAATGCTT CTGAATTTGA
SIN9   1 ---------- ---------- ---------- ---------- ----------
SIN21  1 --AGGCAAAC ACTGAACATT TCAGAGCTAT GAGAATGCTT CTGAATTTGA

SIN4  51 GTTTGCTAGC TCTTGGGGCT GCCTATGTTT CTGCCTTTGC TGTAGAAAAT
SIN7  23 GTTTGCTAGC TCTTGGGGCT GCCTATGTTT CTGCCTTTGC TGTAGAAAAT
SIN9   1 ---------- ---------- ---------- -----TTTGC TGTAGAAAAT
SIN21 49 GTTTGCTAGC TCTTGGGGCT GCCTATGTTT CTGCCTTTGC TGTAGAAAAT

SIN4 101 CCCATGAATA GACTGGTGGC AGAGACCTTG ACACTGCTCT CCACTCATCG
SIN7  73 CCCATGAATA GACTGGTGGC AGAGACCTTG ACACTGCTCT CCACTCATCG
SIN9  16 CCCATGAATA GACTGGTGGC AGAGACCTTG ACACTGCTCT CCACTCATCG
SIN21 99 CCCATCAATA GACTGGTGGC AGAGACCTTG ACACTGCTCT CCACTCATCG

SIN4  151 AACTTGGCTG ATAGGCGATG G---------- ---------- ----------
SIN7  123 AACTTGGCTG ATAGGCGATG G---------- ---------- ----------
SIN9   66 AACTTGGCTG ATAGGCGATG G---------- ---------- ----------
SIN21 149 AACTTGGCTG ATAGGCGATG Gggtaatttt ctttttgatt cctacagtct

SIN4  172 ---------- ---------- ---------- ---------- ----------
SIN7  144 ---------- ---------- ---------- ---------- --
SIN9   87 ---------- ---------- ---------- ---------- ----------
SIN21 199 ttaaaatgca tgggtaattg gtggtggtgg ctagttttta aagatccatt

SIN4  177 ---------- ---------- ---------- ---------- ----------
SIN7  144 ---------- ---------- ---------- ---------- ----------
SIN9   87 ---------- ---------- ---------- ---------- ----------
SIN21 249 atcaataatg aagtaatgag tgttaataat atataatggg taaccatgtt

SIN4  177 ---------- ---------- ---------- ---------- ----------
SIN7  144 ---------- ---------- ---------- ---------- ----------
SIN9   87 ---------- ---------- ---------- ---------- ----------
SIN21 299 actcagaaga attatattaa aagttatgaa ccttacaata catcaaaaat


SIN4  172 ---------- ---------- ----GAACCT GATGATTCCT ACTCCTGAAA
SIN7  144 ---------- ---------- ----GAACCT GATGATTCCT ACTCCTGAAA
SIN9   87 ---------- ---------- ----GAACCT GATGATTCCT ACTCCTGAAA
SIN21 349 gaatgttgtt tcctttcttt ttcaGAACCT GATGATTCCT ACTCCTGAAA

SIN4  198 ATAAAAATCA CCAACTGTGC ATTAAAGAAG TTTTTCAGGG TATAGACACA
SIN7  170 ATAAAAATCA CCAACTGTGC ATTAAAGAAG TTTTTCAGGG TATAGACACA
SIN9  113 ATAAAAATCA CCAACTGTGC ATTAAAGAAG TTTTTCAGGG TATAGACACA
SIN21 399 ATAAAAATCA CCAACTGTGC ATTAAAGAAG TTTTTCAGGG TATAGACACA

SIN4  249 TTGAAGAACC AAACTGCCCA CGGGGAGGCT GTGGATAAAC TATTCCAAAA
SIN7  221 TTGAAGAACC AAACTGCCCA CGGGGAGGCT GTGGATAAAC TATTCCAAAA
SIN9  164 TTGAAGAACC AAACTGCCCA CGGGGAGGCT GTGGATAAAC TATTCCAAAA
SIN21 449 TTGAAGAACC AAACTGCCCA CGGGGAGGCT GTGGATAAAC TATTCCAAAA

SIN4  298 CTTGTCTTTA ATAAAAGAAC ACATAGAGCG CCAAAAAAAA AGGTGTGCAG
SIN7  270 CTTGTCTTTA ATAAAAGAAC ACATAGAGCG CCAAAAAAAA AGGTGTGCAG
SIN9  213 CTTGTCTTTA ATAAAAGAAC ACATAGAGCG CCAAAAAAAA AGGTGTGCAG
SIN21 499 CTTGTCTTTA ATAAAAGAAC ACATAGAGCG CCAAAAAAAA AGGTGTGCAG

SIN4  348 GAGAAAGATG CAGAGTGACA AAGTTCCTAG ACTACCTGCA AGTATTTCTT
SIN7  320 GAGAAAGATG GAGAGTGACA AAGTTCCTAG ACTACCTGCA AGTATTTCTT
SIN9  263 GAGAAAGATG CAGAGTGACA AAGTTCCTAG ACTACCTGCA AGTATTTCTT
SIN21 549 GAGAAAGATG GAGAGTGACA AAGTTCCTAG ACTACCTGCA AGTATTTCTT
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SIN4   398 GGTGTAATAA ACACCGAGTG GACACCGGAA AGTTGAGAAC AAACCGGCTT
SIN7   370 GGTGTAATAA ACACCGAGTG GACACCGGAA AGT------- ----------
SIN9   313 GGTGTAATAA ACACCGAGTG GACACCGGAA AGT------- ----------
SIN21  599 GGTGTAATAA ACACCGAGTG GACACCGGAA AGTTGAGAAC AAACCGGCTT

SIN4   448 ATTGTAGTGG AAGATTTTGG AGAagcatgg ttttttggcg atgagaatga
SIN7   403 ---------- ---------- ---------- ---------- ----------
SIN9   346 ---------- ---------- ---------- ---------- ----------
SIN21  649 ATTGTAGTGG AAGATTTTGG AGA------- ---------- ----------
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Based in the information provided by the Applicants, it should be clear that the disclosed sequences are subsets of each other and are identical in nature in the regions in which they overlap. These fragments may be considered to encode the same protein as the parent and therefore would not constitute an independent invention requiring an independent search. M.P.E.P § 803.04 Therefore, due to the overlapping and identical nature of the fragments, the number of distinct sequences that must be searched and examined would be reduced. In light of the above arguments, Applicants respectfully request the Examiner retract the division of sequences into distinct Inventions and the requirement to elect a particular Invention for examination on the merits.

Respectfully submitted,

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